



## Blast 2 Sequences results

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Taxonomy

Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

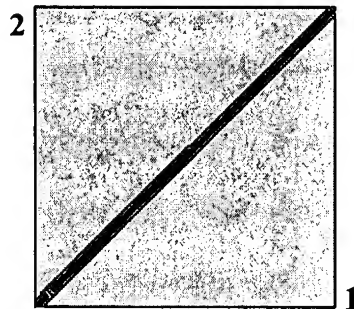
x\_dropoff: 50 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation

Sequence 1: lcl|1\_seq\_1  
Length = 1203 (1 .. 1203)

Sequence 2: lcl|2\_seq\_2  
Length = 1205 (1 .. 1205)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 2072 bits (5368), Expect = 0.0

Identities = 1133/1205 (94%), Positives = 1161/1205 (96%), Gaps = 2/1205 (0%)

Query	1	MGNLKSVAQXXXXXXXXXXXXXXXXXKQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXT	60
		MGNLKS SV QEPGPPCGLGLGLGLGLCGKQGPA+PAPEPSRAPA P AP+HSP + T	
Sbjct	1	MGNLKS SV QEPGPPCGLGLGLGLGLCGKQGPASPAPEPSRAPAPATPHAPDHSPAPNSPT	60
Query	61	--QPPEGPKFPRVKNWEVGSITYDTLSAQAAQDGPCTPRRCLGSLVFPRKLQGRPSGPP	118
		+PPEGPKFPRVKNWE+GSITYDTL AQ+QQDGPCTPR CLGSLV PRKLQ RPSPGPP	
Sbjct	61	LTRPPEGPKFPRVKNWELGSITYDTLCAQSQQDGPCTPRCCLGSLVLPRLQTRPSGPP	120
Query	119	APEQLLSQARDFINQYYSSIKRSGSQAHEQRLQEVEAEVAATGTYQLRESELVFGAKQAW	178
		EQLLSQARDFINQYYSSIKRSGSQAHE+RLQEVEAEVA+TGTY LRESELVFGAKQAW	
Sbjct	121	PAEQLLSQARDFINQYYSSIKRSGSQAHEERLQEVEAEVASTGTYHLRESELVFGAKQAW	180
Query	179	RNAPRCVGRIQWGKLQVFDARDCRSAQEMFTYICNHIKYATNRGNLRSAITVFPQRCPGR	238
		RNAPRCVGRIQWGKLQVFDARDC SAQEMFTYICNHIKYATNRGNLRSAITVFPQR PGR	
Sbjct	181	RNAPRCVGRIQWGKLQVFDARDCSSAQEMFTYICNHIKYATNRGNLRSAITVFPQRAPGR	240

Query	239	GDFRIWNSQLVRYAGYRQODGSGVRGDPANVEITELCIQHWTPGNRFDVLPDLLQAXXX	298
Sbjct	241	GDFRIWNSQLVRYAGYRQODGSGVRGDPANVEITELCIQHWTPGNRFDVLPDLLQAPDE	300
Query	299	XXXXXXXXXXXXXXXXXXXXXXXXXWFAALGLRWYALPAVSNMMLLEIGGLEFPAAFPSGWYM	358
Sbjct	301	PELF+LPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNMMLLEIGGLEF AAPFSGWYM	360
Query	359	STEIGTRNLCDPHRYNILEDVAVCMDDLTRTTSSSLWKDKAAVEINAVLHSYQLAKVTIV	418
Sbjct	361	STEIGTRNLCDPHRYNILEDVAVCMDDLTRTTSSSLWKDKAAVEIN+AVLHS+QLAKVTIV	420
Query	419	DHHAATASFMKHLENEQKARGGCPADWAWIVPPISGSLTPVFHQEMVNYFLSPAIFYQPD	478
Sbjct	421	DHHAAT SFMKHL+NEQKARGGCPADWAWIVPPISGSLTPVFHQEMVNY LSPAIFYQPD	480
Query	479	PWKGSAAKGTGITRKKTFKEVANAVKISASLMGTVMKRVKATILYGSETGRAQSYAQQ	538
Sbjct	481	PWKGSA KG GITRKKTFKEVANAVKISASLMGT+MAKRVKATILY SETGRAQSYAQQ	540
Query	539	GRLFRKAFFDPRVLCMDEYDVVSLEHETLVLVVTSTFGNGDPPENGESFAAALMEMSGPYN	598
Sbjct	541	GRLFRKAFFDPRVLCMDEYDVVSLEHE LVLVVTSTFGNGDPPENGESFAAALMEMSGPYN	600
Query	599	SSPRPEQHKSYSKIRFNSISCSDDLVSWSRRKRKESNTDSAGALGTLRFCVFGLSRAYP	658
Sbjct	601	SSPRPEQHKSYSKIRFNS+SCSDDLVSWSRRKRKESNTDSAGALGTLRFCVFGLSRAYP	660
Query	659	HFCAFAFARVDTRLEELGGERLLQLGQDELGCQEEAFRGWAQAAAFQAACETFCVGEDAKA	718
Sbjct	661	HFCAFAFARVDTRLEELGGERLLQLGQDELGCQEEAFRGWA+AAFQA+CETFCVGE+AKA	720
Query	719	AARDIFSPKRSWKQRQYRLSAQAEGLQLLPGLIHVHRRKMFQATIRSVENLQSSKSTRAT	778
Sbjct	721	AA+DIFSPKRSWKQRQYRLS QAEGQLLPGLIHVHRRKMFQAT+ SVENLQSSKSTRAT	780
Query	779	ILVRLDTGGQEGLOQYQPGDHIGVCPNRPGLVEALLSRVEDPPAPTEPVAVEQLEKGS PG	838
Sbjct	781	ILVRLDT GQEGLOQYQPGDHIG+CPNRPGLVEALLSRVEDPP PTE VAVEQLEKGS PG	840
Query	839	GPPPGWVRDPRLPCTLRQALTFFLDITXXXXXXXXXXXXXXXXXAEPPREQQEALSQDPR	898
Sbjct	841	GPPP WVRDPRLPCTLRQALTFFLDITSPSP+LLRLLSTLAEPP EQQELE LSQDPR	900
Query	899	RYEEWKWFRCPITLLEVLQFQPSVXXXXXXXXXXXXXXXXXRYYSVSSAPSTHPGEIHLTVA	958
Sbjct	901	RYEEWKWFRCPITLLEVLQFQPSVALPAPLLLTQLPLLQPRYYSVSSAP+ HPGE+HLTVA	960
Query	959	VLAYRTQDGLGPLHYGVCSTWLSQLKPGDPVPCFIRGAPSFRLPPDPSLPCILVGP GTGI	1018
Sbjct	961	VLAYRTQDGLGPLHYGVCSTWLSQLK GDPVPCFIRGAPSFRLPPDP +PCILVGP GTGI	1020
Query	1019	APFRGFQWERLHDIESKGLQPTMTLVFGCRCSQLDHLYRDEVQNAQQRGVFGVRLTAFS	1078
Sbjct	1021	APFRGFQWERLHDIESKGLQ PAPMTLVFGCRCSQLDHLYRDEVQDAQERGVFGVRLTAFS	1080
Query	1079	REPDPNPKTYVDILRTELAAEVHRVLCLEGRHMFVCGDVTMATNVLTQTVQRILATEGDME	1138
Sbjct	1081	REPDPNPKTYVDILRTELAAEVHRVLCLEGRHMFVCGDVTMAT+VLQTVQRILATEGDME	1140

```
Query 1139 LDEAGDVIGVLRDQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQERQLRGAVPWAFDPPGS 1198
          LDEAGDVIGVLRDQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQER LRGAVPWAFDPPG
Sbjct 1141 LDEAGDVIGVLRDQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQERHLRGAVPWAFDPPGP 1200

Query 1199 DTNSP 1203
          DT P
Sbjct 1201 DTPGP 1205
```

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda K H  
0.320 0.135 0.423

#### Gapped

Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 10,229

Number of extensions: 6074

Number of successful extensions: 6

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 1203

Length of database: 1,610,148,966

Length adjustment: 147

Effective length of query: 1056

Effective length of database: 1,610,148,819

Effective search space: 1700317152864

Effective search space used: 1700317152864

Neighboring words threshold: 9

X1: 16 ( 7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.8 bits)

S2: 85 (37.4 bits)